

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/S18,072A
Source: IFWB
Date Processed by STIC: 3/27/07

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)**
- 2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
- 3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/518,572A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
 In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> ~~Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses~~
 Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFWO

RAW SEQUENCE LISTING

DATE: 03/27/2007

PATENT APPLICATION: US/10/518,072A

TIME: 16:49:23

Input Set : A:\263365US0XPCT.txt

Output Set: N:\CRF4\03272007\J518072A.raw

3 <110> APPLICANT: Weill, Mylene
 4 Fort, Philippe
 5 Raymond, Michel
 6 Pasteur, Nicole
 8 <120> TITLE OF INVENTION: NOVEL ACETYLCHOLINESTERASE GENE RESPONSIBLE FOR
 9 INSECTICIDE RESISTANCE AND APPLICATIONS THEREOF
 11 <130> FILE REFERENCE: 263365US0XPCT
 13 <140> CURRENT APPLICATION NUMBER: 10/518,072A
 14 <141> CURRENT FILING DATE: 2004-12-16
 16 <150> PRIOR APPLICATION NUMBER: FR 02/07622
 17 <151> PRIOR FILING DATE: 2002-06-20
 19 <150> PRIOR APPLICATION NUMBER: FR 02/13799
 20 <151> PRIOR FILING DATE: 2002-11-05
 23 <160> NUMBER OF SEQ ID NOS: 129
 25 <170> SOFTWARE: PatentIn version 2.1
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 524
 29 <212> TYPE: PRT
 30 <213> ORGANISM: Anopheles gambiae
 32 <400> SEQUENCE: 1
 33 Asp Pro Leu Val Val Asn Thr Asp Lys Gly Arg Ile Arg Gly Ile Thr
 34 1 5 10 15
 36 Val Asp Ala Pro Ser Gly Lys Lys Val Asp Val Trp Leu Gly Ile Pro
 37 20 25 30
 39 Tyr Ala Gln Pro Pro Val Gly Pro Leu Arg Phe Arg His Pro Arg Pro
 40 35 40 45
 42 Ala Glu Lys Trp Thr Gly Val Leu Asn Thr Thr Thr Pro Pro Asn Ser
 43 50 55 60
 45 Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp Phe Pro Gly Ala Thr
 46 65 70 75 80
 49 Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp Cys Leu Tyr Ile Asn
 50 85 90 95
 52 Val Val Ala Pro Arg Pro Arg Pro Lys Asn Ala Ala Val Met Leu Trp
 53 100 105 110
 55 Ile Phe Gly Gly Gly Phe Tyr Ser Gly Thr Ala Thr Leu Asp Val Tyr
 56 115 120 125
 58 Asp His Arg Ala Leu Ala Ser Glu Glu Asn Val Ile Val Val Ser Leu
 59 130 135 140
 61 Gln Tyr Arg Val Ala Ser Leu Gly Phe Leu Phe Leu Gly Thr Pro Glu
 62 145 150 155 160
 64 Ala Pro Gly Asn Ala Gly Leu Phe Asp Gln Asn Leu Ala Leu Arg Trp
 65 165 170 175
 67 Val Arg Asp Asn Ile His Arg Phe Gly Gly Asp Pro Ser Arg Val Thr

Does Not Comply
 Corrected Diskette Needed

(pg. 6)

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DATE: 03/27/2007

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TIME: 16:49:23

Input Set : A:\263365US0XPCT.txt

Output Set: N:\CRF4\03272007\J518072A.raw

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68          180          185          190
70 Leu Phe Gly Glu Ser Ala Gly Ala Val Ser Val Ser Leu His Leu Leu
71          195          200          205
73 Ser Ala Leu Ser Arg Asp Leu Phe Gln Arg Ala Ile Leu Gln Ser Gly
74          210          215          220
76 Ser Pro Thr Ala Pro Trp Ala Leu Val Ser Arg Glu Glu Ala Thr Leu
77 225          230          235          240
79 Arg Ala Leu Arg Leu Ala Glu Ala Val Gly Cys Pro His Glu Pro Ser
80          245          250          255
82 Lys Leu Ser Asp Ala Val Glu Cys Leu Arg Gly Lys Asp Pro His Val
83          260          265          270
85 Leu Val Asn Asn Glu Trp Gly Thr Leu Gly Ile Cys Glu Phe Pro Phe
86          275          280          285
88 Val Pro Val Val Asp Gly Ala Phe Leu Asp Glu Thr Pro Gln Arg Ser
89          290          295          300
91 Leu Ala Ser Gly Arg Phe Lys Lys Thr Glu Ile Leu Thr Gly Ser Asn
92 305          310          315          320
94 Thr Glu Glu Gly Tyr Tyr Phe Ile Ile Tyr Tyr Leu Thr Glu Leu Leu
95          325          330          335
97 Arg Lys Glu Glu Gly Val Thr Val Thr Arg Glu Glu Phe Leu Gln Ala
98          340          345          350
100 Val Arg Glu Leu Asn Pro Tyr Val Asn Gly Ala Ala Arg Gln Ala Ile
101          355          360          365
103 Val Phe Glu Tyr Thr Asp Trp Thr Glu Pro Asp Asn Pro Asn Ser Asn
104          370          375          380
106 Arg Asp Ala Leu Asp Lys Met Val Gly Asp Tyr His Phe Thr Cys Asn
107 385          390          395          400
109 Val Asn Glu Phe Ala Gln Arg Tyr Ala Glu Glu Gly Asn Asn Val Tyr
110          405          410          415
112 Met Tyr Leu Tyr Thr His Arg Ser Lys Gly Asn Pro Trp Pro Arg Trp
113          420          425          430
115 Thr Gly Val Met His Gly Asp Glu Ile Asn Tyr Val Phe Gly Glu Pro
116          435          440          445
118 Leu Asn Pro Thr Leu Gly Tyr Thr Glu Asp Glu Lys Asp Phe Ser Arg
119          450          455          460
121 Lys Ile Met Arg Tyr Trp Ser Asn Phe Ala Lys Thr Gly Asn Pro Asn
122 465          470          475          480
124 Pro Asn Thr Ala Ser Ser Glu Phe Pro Glu Trp Pro Lys His Thr Ala
125          485          490          495
127 His Gly Arg His Tyr Leu Glu Leu Gly Leu Asn Thr Ser Phe Val Gly
128          500          505          510
130 Arg Gly Pro Arg Leu Arg Gln Cys Ala Phe Trp Lys
131          515          520
135 <210> SEQ ID NO: 2
136 <211> LENGTH: 1932
137 <212> TYPE: DNA
138 <213> ORGANISM: Anopheles gambiae
140 <220> FEATURE:
141 <221> NAME/KEY: CDS

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Input Set : A:\263365US0XPCT.txt

Output Set: N:\CRF4\03272007\J518072A.raw

142 <222> LOCATION: (1)..(1932)

144 <400> SEQUENCE: 2

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145 atg ttt gtg tgt tgt ttt ttc ttt ctc tct ctc tct ttc tgt ggt tcc 48
146 Met Phe Val Cys Cys Phe Phe Phe Leu Ser Leu Ser Phe Cys Gly Ser
147 1 5 10 15
149 aac att tca gac gca ttt ttt aca cca tat ata ggt cac ggt gag tcc 96
150 Asn Ile Ser Asp Ala Phe Phe Thr Pro Tyr Ile Gly His Gly Glu Ser
151 20 25 30
153 gta cga att ata gat gcc gag ttg ggc acg ctc gag cat gtc cac agt 144
154 Val Arg Ile Ile Asp Ala Glu Leu Gly Thr Leu Glu His Val His Ser
155 35 40 45
157 gga gca acg ccg cgg cga cgc ggc ctg acg agg cgc gag tca aac tcg 192
158 Gly Ala Thr Pro Arg Arg Arg Gly Leu Thr Arg Arg Glu Ser Asn Ser
159 50 55 60
161 gac gcg aac gac aac gat ccg ctg gtg gtc aac acg gat aag ggg cgc 240
162 Asp Ala Asn Asp Asn Asp Pro Leu Val Val Asn Thr Asp Lys Gly Arg
163 65 70 75 80
165 atc cgc ggc att acg gtc gat gcg ccc agc ggc aag aag gtg gac gtg 288
166 Ile Arg Gly Ile Thr Val Asp Ala Pro Ser Gly Lys Lys Val Asp Val
167 85 90 95
169 tgg ctc ggc att ccc tac gcc cag ccg ccg gtc ggg ccg cta cgg ttc 336
170 Trp Leu Gly Ile Pro Tyr Ala Gln Pro Pro Val Gly Pro Leu Arg Phe
171 100 105 110
173 cgt cat ccg cgg ccg gcc gaa aag tgg acc ggc gtg ctg aac acg acc 384
174 Arg His Pro Arg Pro Ala Glu Lys Trp Thr Gly Val Leu Asn Thr Thr
175 115 120 125
177 aca ccg ccc aac agc tgc gtg cag atc gtg gac acc gtg ttc ggc gac 432
178 Thr Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp
179 130 135 140
181 ttc ccg ggc gcg acc atg tgg aac ccg aac acg ccc ctg tcc gag gac 480
182 Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp
183 145 150 155 160
185 tgt ctg tac att aac gtg gtg gca ccg cga ccc cgg ccc aag aat gcg 528
186 Cys Leu Tyr Ile Asn Val Val Ala Pro Arg Pro Arg Pro Lys Asn Ala
187 165 170 175
189 gcc gtc atg ctg tgg atc ttc ggc ggc ggc ttc tac tcc ggc acc gcc 576
190 Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly Thr Ala
191 180 185 190
193 acc ctg gac gtg tac gac cac ccg gcg ctt gcg tcg gag gag aac gtg 624
194 Thr Leu Asp Val Tyr Asp His Arg Ala Leu Ala Ser Glu Glu Asn Val
195 195 200 205
197 atc gtg gtg tcg ctg cag tac cgc gtg gcc agt ctg ggc ttc ctg ttt 672
198 Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe Leu Phe
199 210 215 220
201 ctc ggc acc ccg gaa gcg ccg ggc aat gcg gga ctg ttc gat cag aac 720
202 Leu Gly Thr Pro Glu Ala Pro Gly Asn Ala Gly Leu Phe Asp Gln Asn
203 225 230 235 240
205 ctt gcg cta cgc tgg gtg ccg gac aac att cac ccg ttc ggt ggc gat 768
206 Leu Ala Leu Arg Trp Val Arg Asp Asn Ile His Arg Phe Gly Gly Asp

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Input Set : A:\263365US0XPCT.txt

Output Set: N:\CRF4\03272007\J518072A.raw

207		245		250		255	
209	ccg tcg cgt gtg aca ctg ttc ggc gag agt gcc ggt gcc gtc tcg gtg						816
210	Pro Ser Arg Val Thr Leu Phe Gly Glu Ser Ala Gly Ala Val Ser Val						
211		260		265		270	
213	tcg ctg cat ctg ctg tcc gcc ctt tcc cgc gat ctg ttc cag cgg gcc						864
215	Ser Leu His Leu Leu Ser Ala Leu Ser Arg Asp Leu Phe Gln Arg Ala						
216		275		280		285	
218	atc ctg cag agc ggc tcg ccg acg gca ccg tgg gca ttg gta tcg cgc						912
219	Ile Leu Gln Ser Gly Ser Pro Thr Ala Pro Trp Ala Leu Val Ser Arg						
220		290		295		300	
222	gag gaa gcc aca cta aga gca ctg cgg ttg gcc gag gcg gtc ggc tgc						960
223	Glu Glu Ala Thr Leu Arg Ala Leu Arg Leu Ala Glu Ala Val Gly Cys						
224	305		310		315		320
226	ccg cac gaa ccg agc aag ctg agc gat gcg gtc gag tgc ctg cgc ggc						1008
227	Pro His Glu Pro Ser Lys Leu Ser Asp Ala Val Glu Cys Leu Arg Gly						
228		325		330		335	
230	aag gac ccg cac gtg ctg gtc aac aac gag tgg ggc acg ctc ggc att						1056
231	Lys Asp Pro His Val Leu Val Asn Asn Glu Trp Gly Thr Leu Gly Ile						
232		340		345		350	
234	tgc gag ttc ccg ttc gtg ccg gtg gtc gac ggt gcg ttc ctg gac gag						1104
235	Cys Glu Phe Pro Phe Val Pro Val Val Asp Gly Ala Phe Leu Asp Glu						
236		355		360		365	
238	acg ccg cag cgt tcg ctc gcc agc ggg cgc ttc aag aag acg gag atc						1152
239	Thr Pro Gln Arg Ser Leu Ala Ser Gly Arg Phe Lys Lys Thr Glu Ile						
240		370		375		380	
242	ctc acc ggc agc aac acg gag gag ggc tac tac ttc atc atc tac tac						1200
243	Leu Thr Gly Ser Asn Thr Glu Glu Gly Tyr Tyr Phe Ile Ile Tyr Tyr						
244	385		390		395		400
246	ctg acc gag ctg ctg cgc aag gag gag ggc gtg acc gtg acg cgc gag						1248
247	Leu Thr Glu Leu Leu Arg Lys Glu Glu Gly Val Thr Val Thr Arg Glu						
248		405		410		415	
250	gag ttc ctg cag gcg gtg cgc gag ctc aac ccg tac gtg aac ggg gcg						1296
251	Glu Phe Leu Gln Ala Val Arg Glu Leu Asn Pro Tyr Val Asn Gly Ala						
252		420		425		430	
254	gcc ccg cag gcg atc gtg ttc gag tac acc gac tgg acc gag ccg gac						1344
255	Ala Arg Gln Ala Ile Val Phe Glu Tyr Thr Asp Trp Thr Glu Pro Asp						
256		435		440		445	
258	aac ccg aac agc aac ccg gac gcg ctg gac aag atg gtg ggc gac tat						1392
259	Asn Pro Asn Ser Asn Arg Asp Ala Leu Asp Lys Met Val Gly Asp Tyr						
260		450		455		460	
262	cac ttc acc tgc aac gtg aac gag ttc gcg cag ccg tac gcc gag gag						1440
263	His Phe Thr Cys Asn Val Asn Glu Phe Ala Gln Arg Tyr Ala Glu Glu						
264	465		470		475		480
266	ggc aac aac gtc tac atg tat ctg tac acg cac cgc agc aaa ggc aac						1488
267	Gly Asn Asn Val Tyr Met Tyr Leu Tyr Thr His Arg Ser Lys Gly Asn						
268		485		490		495	
270	ccg tgg ccg cgc tgg acg ggc gtg atg cac ggc gac gag atc aac tac						1536
271	Pro Trp Pro Arg Trp Thr Gly Val Met His Gly Asp Glu Ile Asn Tyr						
272		500		505		510	

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Input Set : A:\263365US0XPCT.txt

Output Set: N:\CRF4\03272007\J518072A.raw

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274 gtg ttc ggc gaa ccg ctc aac ccc acc ctc ggc tac acc gag gac gag 1584
275 Val Phe Gly Glu Pro Leu Asn Pro Thr Leu Gly Tyr Thr Glu Asp Glu
276      515      520      525
278 aaa gac ttt agc cgg aag atc atg cga tac tgg tcc aac ttt gcc aaa 1632
279 Lys Asp Phe Ser Arg Lys Ile Met Arg Tyr Trp Ser Asn Phe Ala Lys
280      530      535      540
282 acc ggg aat cca aat ccc aac acg gcc agc agc gaa ttc ccc gag tgg 1680
283 Thr Gly Asn Pro Asn Pro Asn Thr Ala Ser Ser Glu Phe Pro Glu Trp
284 545      550      555      560
286 ccc aag cac acc gcc cac gga cgg cac tat ctg gag ctg ggc ctc aac 1728
287 Pro Lys His Thr Ala His Gly Arg His Tyr Leu Glu Leu Gly Leu Asn
288      565      570      575
291 acg tcc ttc gtc ggt cgg ggc cca cgg ttg agg cag tgt gcc ttc tgg 1776
292 Thr Ser Phe Val Gly Arg Gly Pro Arg Leu Arg Gln Cys Ala Phe Trp
293      580      585      590
295 aag aag tac ctt ccc cag cta gtt gca gct acc tcg aac cta cca ggg 1824
296 Lys Lys Tyr Leu Pro Gln Leu Val Ala Ala Thr Ser Asn Leu Pro Gly
297      595      600      605
299 cca gca ccg cct agt gaa ccg tgc gaa agc agc gca ttt ttt tac cga 1872
300 Pro Ala Pro Pro Ser Glu Pro Cys Glu Ser Ser Ala Phe Phe Tyr Arg
301      610      615      620
303 cct gat ctg atc gtg ctg ctg gtg tcg ctg ctt acg gcg acc gtc aga 1920
304 Pro Asp Leu Ile Val Leu Leu Val Ser Leu Leu Thr Ala Thr Val Arg
305 625      630      635      640
307 ttc ata caa taa 1932
308 Phe Ile Gln
311 <210> SEQ ID NO: 3
312 <211> LENGTH: 643
313 <212> TYPE: PRT
314 <213> ORGANISM: Anopheles gambiae
316 <400> SEQUENCE: 3
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318 1      5      10      15
320 Asn Ile Ser Asp Ala Phe Phe Thr Pro Tyr Ile Gly His Gly Glu Ser
321      20      25      30
323 Val Arg Ile Ile Asp Ala Glu Leu Gly Thr Leu Glu His Val His Ser
324      35      40      45
326 Gly Ala Thr Pro Arg Arg Arg Gly Leu Thr Arg Arg Glu Ser Asn Ser
327      50      55      60
329 Asp Ala Asn Asp Asn Asp Pro Leu Val Val Asn Thr Asp Lys Gly Arg
330 65      70      75      80
332 Ile Arg Gly Ile Thr Val Asp Ala Pro Ser Gly Lys Lys Val Asp Val
333      85      90      95
335 Trp Leu Gly Ile Pro Tyr Ala Gln Pro Pro Val Gly Pro Leu Arg Phe
336      100      105      110
338 Arg His Pro Arg Pro Ala Glu Lys Trp Thr Gly Val Leu Asn Thr Thr
339      115      120      125
341 Thr Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp
342      130      135      140

```

<210> SEQ ID NO 128
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (6)..(6)
<223> OTHER INFORMATION: n=a,c,g, or t
<400> SEQUENCE: 128
ccgggngcsa cyatgtggaa

20

↑
See item #11 on error
summary sheet.

↑
The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/518,072A

DATE: 03/27/2007
TIME: 16:49:24

Input Set : A:\263365US0XPCT.txt
Output Set: N:\CRF4\03272007\J518072A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:128; N Pos. 6 ✓

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:39,40,41,42,43,44,45,46,47,48,49,50,54,55,58,59,123,124,128,129

VERIFICATION SUMMARY

DATE: 03/27/2007

PATENT APPLICATION: US/10/518,072A

TIME: 16:49:24

Input Set : A:\263365US0XPCT.txt

Output Set: N:\CRF4\03272007\J518072A.raw

L:6024 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:128 after pos.:0